BLAST Basic Local Alignment Search Tool

-

Blast 2 sequences

AJ242652:Hepatitis C virus replicon I377/NS3-3'UTR

Results for: emb|AJ242652.1 Hepatitis C virus replicon I377/NS3-3'UTR(7989bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
gi|5441834|emb|AJ242652.1|
Description
Hepatitis C virus replicon I377/NS3-3'UTR
Molecule type
nucleic acid
Query Length
7989

Subject ID
29035
Description
None
Molecule type
nucleic acid
Subject Length
9599
Program
BLASTN 2.2.21+ Citation

Reference
Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences",
J Comput Biol 2000; 7(1-2):203-14.
Other reports: Search Summary [Taxonomy reports]

Search Parameters

Program	blastn
Word size	28
Expect value	10
Hitlist size	100
Match/Mismatch scores	1,-2
Gapcosts	0,0
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Karlin-Altschul statistics

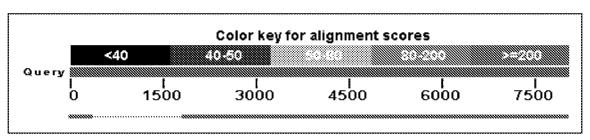| Params	Ungapped	Gapped
Lambda	1.33271	1.28
K	0.620991	0.46
H	1.12409	0.85

Results Statistics

Distribution of 2 Blast Hits on the Query Sequence

[?] _____

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

Plot of gi|5441834|emb|AJ242652.1| vs 29035 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

Descriptions

Legend for links to other resources: [U] UniGene [E] GEO [G] Gene [S] Structure [M] Map Viewer

Sequences producing significant alignments:
(Click headers to sort columns)

29035	4447	5111	82%	0.0	98%

>lcl|29035
Length=9599

```
 Score = 4447 bits (2408),  Expect = 0.0
 Identities = 5058/6316 (80%), Gaps = 268/6316 (4%)
 Strand=Plus/Plus

Query  1802   TGGCGCCTATTACGGCCTACTCCCAACAGACGCGAGGCCTACTTGGCTGCATCATCACTA   1861
              || |||| | ||| || ||| |||| ||||| || ||||| |  ||  | |||| |||| |
Sbjct  3418   TGGCGCCCATCACGGCGTACGCCCAGCAGACGAGAGGCCTCCTAGGGTGTATAATCACCA   3477

Query  1862   GCCTCACAGGCCGGGACAGGAACCAGGTCGAGGGGGAGGTCCAAG-TGGTCTCCACCGCA   1920
              |||| ||| |||||||||| ||||| ||||| ||  || ||| | ||  |  || || ||
Sbjct  3478   GCCTGACTGGCCGGGACAAAAACCAAGTGGAGGGTGAGGTCC-AGATCGTGTCAACTGCT   3536

Query  1921   ACACAATCTTTCCTGGCGACCTGCGTCAATGGCGTGTGTTGGACTGTCTATCATGGTGCC   1980
              || |||| || ||||||  |  || || ||||   || | |||||||||| ||| || |||
Sbjct  3537   ACCCAAACCTTCCTGGCAACGTGCATCAATGGGGTATGCTGGACTGTCTACCACGGGGCC   3596

Query  1981   GGCTCAAAGACCCTTGCCGGC-CCAAAGGGCCCAATCACCCAAATGTACACCAATGTGGA   2039
              ||  |  | ||||| |  | | |||| ||| ||  | ||| ||||| ||| || ||||||
Sbjct  3597   GGAACGAGGACCATCG-CATCACCCAAGGGTCCTGTCATCCAGATGTATACCAATGTGGA   3655

Query  2040   CCAGGACCTCGTCGGCTGGCAAGCGCCCCCCGGGGCGCGTTCCTTGACACCATGCACCTG   2099
              ||| |||| | || ||||||| || ||   ||  ||  || |||||||| |  ||| |||
Sbjct  3656   CCAAGACCTTGTGGGCTGGCCCGCTCCTCAAGGTTCCCGCTCATTGACACCCTGTACCTG   3715

Query  2100   CGGCAGCTCGGACCTTTACTTGGTCACGAGGCATGCCGATGTCATTCCGGTGCGCCGGCG   2159
              |||| | || |||||||| ||||||||||||| ||||||||||||| |||||||||||||
Sbjct  3716   CGGCTCCTCGGACCTTTACCTGGTCACGAGGCACGCCGATGTCATTCCCGTGCGCCGGCG   3775

Query  2160   GGGCGACAGCAGGGGGAGCCTACTCTC-CCCCAGGCCCGTCTCCTACTTGAAGGGCTCTT   2218
               ||  | | | || ||||||| | |   | || |||  |  || |||||||| |||| |
Sbjct  3776   AGGTGATAGCAGGGGTAGCCTGCTTTCGCCCC-GGCCCATTTCCTACTTGAAAGGCTCCT   3834

Query  2219   CGGGCGGTCCACTGCTCTGCCCCTCGGGGCACGCTGTGGGCATCT-TTC-GGGCTGCCGT   2276
              || |  ||| ||||  | |||||| || | || | |  |||  |  ||| |||||||||
Sbjct  3835   CGGGGGGTCCGCTGTTGTGCCCCGCGGGACACGCCGTGGGC--CTATTCAGGGCCGCGGT   3892

Query  2277   GTGCACCCGAGGGGGTTGCGAAGGCGGTGGACTTTGTACCC-GTCGAG--TCTATGGAAAC   2333
              |||||||||  | ||| | |||| |||||||||| | ||| ||| |   ||| | ||  |
Sbjct  3893   GTGCACCCGTGGAGTGGCTAAAGCGGTGGACTTTAT-CCCTGTGGAGAACCTA-GG-GAC   3949

Query  2334   CACTATGCGGTCCCCGGTCTTCACGGACAACTCGTCCCCTCCGGCCGTACCGCAGA-CAT   2392
               || |||| ||| ||||| ||||||||||||| |  |  || ||| || ||  ||| ||
Sbjct  3950   AACCATGAGATCCCCGGTGTTCACGGACAACTCCTCTCCACCAGCAGTGCCCCAGAGC-T   4008

Query  2393   TCCAGGTGGCCCATCTACACGC-CCCTACTGGTAGCGGCAAGAGCACTAAGGTGCCGGCT   2451
              |||||||||||||| ||| || | || | |||| ||||| |||||||| |||| |||||
Sbjct  4009   TCCAGGTGGCCCACCTGCATGCTCCC-ACCGGCAGCGGTAAGAGCACCAAGGTCCCGGCT   4067

Query  2452   GCGTATGCAGCCCAAGGG-TATAAGGTGCTT-GTCCTGAACCCGTCCGTCGCCGCCACCC   2509
              ||||| |||||   ||| |||  |||| |   || ||||||| | | ||  |  | ||
Sbjct  4068   GCGTACGCAGCCC-AGGGCTACAAGGTG-TTGGTGCTCAACCCCTCTGTTGCTGCAACGC   4125

Query  2510   TAGG-TTTCGGGGCGTATATGTCTAAGGCACATGGTATCGACCCTAACATCAGAACCGGG   2568
              | || ||| |  ||| || |||  |||||| |||| |||||||| || |||||| | |||
Sbjct  4126   TGGGCTTTT-GGTGCTTACATGTCCAAGGCCCATGGGGTTGATCCTAATATCAGGACCGGG   4184

Query  2569   GTAAGGACCATCACCAC-GGGTGCCCCCATCACGTACTCCACCTATGGCAAGTTTCTTGC   2627
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           ||| || || |||||||| |||   |||      || ||  ||||||||  ||| | || ||||||
Sbjct  4185  GTGAGAACAATTACCACTGGCAG-CCCCATCACGTACTCCACCTACGGCAAGTTCCTTGC  4243

Query  2628  CGACGGTGGTTGCTCTGGGGGCGCCTATGACATCATAATATGTGATGAGTGCCACTCAAC  2687
             |||||| ||  || ||||  ||   |||||||| || ||  ||||||| ||||||||| |
Sbjct  4244  CGACGGCGGGTGCTCAGGAGGTGCTTATGACATAATAATTTGTGACGAGTGCCACTCCAC  4303

Query  2688  TGACTCGACCAC-T--ATCCTGGGCATCGGCACAGTCCTGGACCAAGCGGAGACGGCTGG  2744
              |||| | ||   |  ||||||||||||||||| ||||||||||||||| || || ||||
Sbjct  4304  GGA-T-G-CCACATCCATCTTGGGCATCGGCACTGTCCTTGACCAAGCAGAGACTGCGGG  4360

Query  2745  AGCGCGACTCGTCGTGCTCGCCACCGCTACGCCTCCGGGATCGGTCACCGTG-CCACATC  2803
              ||| ||||| || ||||||||||| |||| |||| ||||| ||||||| ||  || ||||
Sbjct  4361  GGCGAGACTGGTTGTGCTCGCCACTGCTACCCCTCCGGGCTCCGTCACTGTGTCC-CATC  4419

Query  2804  CAAACATCGAGGAGGTGGCTCTGTCCAGCACTGGAGAAATCCCCTTTTATGGCAAAGCCA  2863
              ||| |||||||||| | |||||||||| | || ||||| ||||||| | ||||| || |
Sbjct  4420  CTAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCCTTTTACGGCAAGGCTA  4479

Query  2864  TCCCCATCGAGACCATCAAgggggggAGGCACCTCATTTTCTGCCATTCCAAGAAGAAAT  2923
              ||||| ||||| | |||||||   || ||| ||| || |||||||| |||||||||| |
Sbjct  4480  TCCCCCTCGAGGTGATCAAGGGGGGGAAGACATCTCATCTTCTGCCACTCAAAGAAGAAGT  4539

Query  2924  GTGATGAGCTCGCCGCGAAGCT-GTCCGGCCTCGGAC-TCAATGCTGTAGCATATTACCG  2981
              | || ||||||||||||||||| ||| | | ||| | |||| ||  || ||| ||||||
Sbjct  4540  GCGACGAGCTCGCCGCGAAGCTGGT-C-GCATTGGGCATCAATGCCGTGGCCTACTACCG  4597

Query  2982  GGGCCTTGATGTATCCGTCATACCAACTAGCGGAGACGTCATTGTCGTAG-CAACGGACG  3040
              ||| |||||||| |||||||| || ||||| |||| |||| ||||| || | || || |
Sbjct  4598  CGGTCTTGACGTGTCTGTCATCCCGACCAGCGGCGATGTTGTCGTCGT-GTCGACCGATG  4656

Query  3041  CTCTAATGACGGGCTTTACCGGCGATTTCGACTCAGTGATCGACTGCAATACATGTGTCA  3100
              ||||| ||||| ||||||||||||| ||||||||| |||| ||||||||||| |||||||
Sbjct  4657  CTCTCATGACTGGCTTTACCGGCGACTTCGACTCTGTGATAGACTGCAACACGTGTGTCA  4716

Query  3101  CCCAGACAGTCGACTTCAGCCTGGACCCGACCTTCACCATTGAGACGACGACCG-TGCCA  3159
              | |||||||||||| |||||||| |||| |||||||||||||||||| || |  |||| |
Sbjct  4717  CTCAGACAGTCGATTTCAGCCTTGACCCTACCTTTACCATTGAGACAACCA-CGCTCCCC  4775

Query  3160  CAAGACGCGGTGT-CACGCTCGCAGCGGCGAGGCAGGACTGGTAGGGGCAGGATGGGCAT  3218
              ||| | || ||   ||  |  |||| |||||||||||||||||| || | |||| |||||
Sbjct  4776  CAGGATGCTGTCTCCA-GGACTCAACGCCGGGGCAGGACTGGCAGGGGGAAGCCAGGCAT  4834

Query  3219  TTACAGGTTTGTGACTCCAGGAGAACGGCCCTCGGGCATGTTCGATTCCTCGGTTCTGTG  3278
              |||| ||||||||| || ||||| |||| ||||||||||||||||| | || |  | |||
Sbjct  4835  CTATAGATTTGTGGCACCGGGGGGAGCGCCCCTCCGGCATGTTCGACTCGTCCGTCCTCTG  4894

Query  3279  CGAGTGCTATGACGCGGGCTGTGCTTGGTACGAGCTCACGCCCGCCGAGACCT-CAGTTA  3337
              ||||||||||||||||||||||||||||||| |||||||||||||||||||| |||||||
Sbjct  4895  TGAGTGCTATGACGCGGGCTGTGCTTGGTATGAGCTCACGCCCGCCGAGAC-TACAGTTA  4953

Query  3338  GGTTGCGGGCTTACCTAAACACACCAGGG-TTGCCCGTCTGCCAGGACCATCTGGAGTTC  3396
              ||| | || || | |  ||  |||| ||| |||  |||||||||||||||||| |||| |
Sbjct  4954  GGCTACGAGCGTACATGAACACCCCGGGGCTT-CCCGTGTGCCAGGACCATCTTGAATTT  5012

Query  3397  TGGGAGAGCGTCTTTACAGGCCTCACCCACATAGACGCCCA-TTTCTTGTCCCAGACTAA  3455
              |||||| ||||||||||| ||||||||  ||||||| |||| ||| |  |||||||| ||
Sbjct  5013  TGGGAGGGCGTCTTTACGGGCCTCACTCATATAGATGCCCACTTT-TTATCCCAGACAAA  5071

Query  3456  GCAG-GCAGGAGACAACTTCCCCTACCTGGTAGCATACCAGGCTACGGTGTGCGCCAGGG  3514
              |||| ||||  | ||||| || ||||||||||||| ||||| || |||||||||| ||||
Sbjct  5072  GCAGAGTGGG-GAGAACTTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCTAGGG  5130

Query  3515  CTCAGGCTCCACCTCCATCGTGGGACCAAATGTGGAAGTGTCTCATACGGCT-AAAGCCT  3573
              ||||| ||  || |||||||||||||||| ||||||||||| |   |||| | ||| |
Sbjct  5131  CTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATCCGCCTTAAACCC-  5189

Query  3574  ACGCTGCACGGGCCAACGCCCCTGCTGTATAGGCTGGGAGCCGTTCAAAACGAGGTTACT  3633
              || || ||| ||||||| ||||||||||| | ||||| || |||||||| || |  ||
Sbjct  5190  ACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAGTCAC-  5248

Query  3634  ACC--ACACACCCCATAACCAAATACATCATGGCATGCATGTCGGCTGACCTGGAGGTCG  3691
              |||    ||| |||||| ||||||||||||||| |||||||||||| ||||||||||||
Sbjct  5249  -CCTGACGCACCCAATCACCAAATACATCATGACATGCATGTCGGCCGACCTGGAGGTCG  5307

Query  3692  TCACGAGCACCTGGGTGCTGGTAGGCGGAGTCCTAGCAGCTCTGGCCGCGTATTGCCTGA  3751
              |||||||||||||||||||| | ||||| |||||||| || ||||||||||||||||||
Sbjct  5308  TCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTCTGGCCGCGTATTGCCTGT  5367

Query  3752  CAACAGGCAGCGTGGTCATTGTGGGCAGGATCATCTTGTCCGGAAAGCCGGCCATCATTC  3811
              |||||||| |||||||||| | ||||||||||| ||||||||||||||||||| ||  ||
Sbjct  5368  CAACAGGCTGCGTGGTCATAGTGGGCAGGATCGTCTTGTCCGGGAAGCCGGCAATTATAC  5427
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http://blast.ncbi.nlm.nih.gov/Blast.cgi NCBI Blast:AJ242652:Hepatitis C virus replicon I377/NS3-3'UTR

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Query  3812  CCGACAGGGAAGTCCTTTACCGGGAGTTCGATGAGATGGAAGAGTGCGCCTCA-CACCTC  3870
             | |||||||||| || || ||||| |||||||||||||||||||||| | ||| ||
Sbjct  5428  CTGACAGGGAGGTTCTCTACCAGGAGTTCGATGAGATGGAAGAGTGCTC-TCAGCACTTA  5486

Query  3871  CCTTACATCGAACA-GGGAATGCA-GCTCGCCGAACAATTCAAACAGAAGGCAATCGGGT  3928
             || |||||||| || |||| || | |||||| ||||| |||||| ||||||| || |||
Sbjct  5487  CCGTACATCGAGCAAGGGA-TG-ATGCTCGCTGAGCAGTTCAAGCAGAAGGCCCTCGGCC  5544

Query  3929  TGCTGCAAACAGCCACCAAGCAA-GCGGAGGCTGCTGCTCCCGTGGTGG--A-ATCCAAG  3984
             | ||||| ||| || ||  || | ||  || || |||  || |||| ||  | | || ||
Sbjct  5545  TCCTGCAGACCGCGTCCC-GCCATGCAGAGGTTA-T-CACCCCTGCTGTCCAGA-CCAAC  5600

Query  3985  TGGCGGACCCTCGAAGCCTTCTGGGCGAAGCATATGTGGAATTTCATCAGCGGGATACAA  4044
             ||||  | | |||| |||| |||||||||||| |||||||||||||||||| ||||||||
Sbjct  5601  TGGCAGAAACTCGAGGTCTTTTGGGCGAAGCACATGTGGAATTTCATCAGTGGGATACAA  5660

Query  4045  TATTTAGCAGGCTTGTCCACTCTGCCTGGCAACCCCGCGATAGCATCACTGATGGCATTC  4104
             ||  || || ||| |||| | || |||||  ||||||| ||  |  ||| ||||||  |
Sbjct  5661  TACTTGGCGGGCCTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTT  5720

Query  4105  ACAGCCT-CTATCACCAGCCCGCTCACCACCCAACATACCCTCCTGTTTAACATCCTGGG  4163
             ||||| | || ||||||||| || | ||||| ||| | ||||||| | | ||||| |||
Sbjct  5721  ACAGC-TGCCGTCACCAGCCCACTAACCACTGGCCAAACCCTCCTCTTCAACATATTGGG  5779

Query  4164  GGGATGGGTGGCCGCCCAACTTGCT-CCTCCCAGCGCTGCTTCTGC-TTTCGTAGGCGCC  4221
             ||| ||||||| || |||||| || | || | |||| ||| | ||| || |||  |||
Sbjct  5780  GGGGTGGGTGGCTGCCCAGCTCGCCGCC-CCCGGTGCCGCTACTGCCTTT-GTGGGTGCT  5837

Query  4222  GGCATCGCTGGAGCGGCTGTTGGCAGCATAGGCCTTGGGAAGGTGCTTGTGGATATT-TT  4280
             ||| | || || || |   | |||||| | || ||||||||||| ||  |||| | | ||
Sbjct  5838  GGCCTAGCTGGCGCCGCCATCGGCAGCGTTGGACTGGGGAAGGTCCTCGTGGACATTCTT  5897

Query  4281  GGCAGGTTATGGAGCAGGG-GTGGCAGGCGCGCTCGTGGCCTTTAAGGTCATGAGCGGCG  4339
             || || | ||||| | || ||  | || |  |||  | | || | || |||||||||| |
Sbjct  5898  G-CAGGGTATGGCGC-GGGCGTGGCGGGAGCTCTTGTAGCATTCAAGATCATGAGCGGTG  5955

Query  4340  AGATGCCCTCCACCGAGGACCTGGTTAACCTACT-CCCTGCTATCCTCTCCCCTGGCGCC  4398
             | | ||||||||| ||||||||||||||  | || ||| || |||||||| ||||| |||
Sbjct  5956  AGGTCCCCTCCACGGAGGACCTGGTCAATCTGCTGCCC-GCCATCCTCTCGCCTGGAGCC  6014

Query  4399  CTAGTCGTCGGGGTCGTGTGCGCAGCGATACTGCGTCGGCACGTGGGCCCAGGG-GAGGG  4457
             || |||||| |  | |||| |||||||| |||||||| | ||||| |||| ||| ||||||
Sbjct  6015  CTTGTAGTCGGTGTGGTCTGCGCAGCAATACTGCGCCGGCACGTTGGCCC-GGGCGAGGG  6073

Query  4458  GGCTGTGCAGTGGATGAACCGGCTGATAGCGTTCGCTTCGCGGGGTAACCACGTCTCCCC  4517
             ||| ||||| ||||||||||||||| || ||||||| | || |  ||||| ||| ||||
Sbjct  6074  GGCAGTGCAATGGATGAACCGGCTAATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCC  6133

Query  4518  CACGCACTATGTGCCTGAGAGCGACGCTGCAGCACGTGTCACT-CAGATCCTCT-CTAGT  4575
             |||||||| ||||| || ||||||| | |||||| |||||||| || | |   | | ||
Sbjct  6134  CACGCACTACGTGCCGGAGAGCGATGCAGCCGCCCGCGTCACTGCC-ATACTCAGC-AGC  6191

Query  4576  CTTACCATCACTCAGCTGCTGAAGAGGCTTCACCAGTGGATCAA-CGAGGACTGCT-CCA  4633
             || || || | | |||| ||||| ||| | ||| ||||| |  | || | |   | |||
Sbjct  6192  CTCACTGTAACCCAGCTCCTGAGGCGACTGCATCAGTGGAT-AAGCTCGGAGTG-TACCA  6249

Query  4634  CGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTGGATATGC-ACGGTGTTGA-C  4691
             | |||||||||| || ||||||||| || | ||| ||||| |||||||| || | | |
Sbjct  6250  CTCCATGCTCCGGTTCCTGGCTAAGGGACATCTGGGACTGGATATGCGA-GGTGCTGAGC  6308

Query  4692  TGA-TTTCAAGACCTGGCTCCA-GTCCAAGCTCCTGCCGCGATTGCC-GGGAGTCCCCTT  4748
             | | ||| |||||||||||  | |||||||||   || || ||| || ||||| | ||||
Sbjct  6309  -GACTTT-AAGACCTGGCTGAAAG-CCAAGCTCATGCCACAACTGCCTGGGATTCCCTTT  6365

Query  4749  CT-TCTCATGTCAACGTGGGTACAAGGGAGTCTGGCGGGGCGACGGCATCATGCAAAC-C  4806
             | | ||| ||  |||| |||| ||||||| |||||| | |||||| |||| |||| | |
Sbjct  6366  GTGTC-C-TGCCAGCGCGGGTATAGGGGGGTCTGGCGAGGAGACGGCATTATGCACACTC  6423

Query  4807  ACCTGCC-CATGTGGAGCACAGATCACCGGACATGTGAAAAACGGTTCCATGAGGATCGT  4865
             | ||||| ||||||||||| ||||||| ||||||||||||| || || |||||||||||
Sbjct  6424  GC-TGCCAC-TGTGGAGCTGAGATCACTGGACATGTCAAAAACGGGACGATGAGGATCGT  6481

Query  4866  GGGGCCTAGGACCTGTAGTAACACGTGGCA-TGGAACATTCCCCATTAACGCGTACACCA  4924
             || ||||||||||| |||  ||||||||| | |||| |||||||||||||||| |||||||
Sbjct  6482  CGGTCCTAGGACCTGCAGGAACATGTGG-AGTGGGACGTTCCCCATTAACGCCTACACCA  6540

Query  4925  CGGGCCCCTGCACGCCC-TCCCCGGCGCCAAATTATTC-TAGGGCGCTGTGGCGGGTGGC  4982
             |||||||||||| | || ||||| |||| | |||| || | || ||| ||||| ||||| |
Sbjct  6541  CGGGCCCCTGTACTCCCCTTCCTG-CGCCGAACTATAAGTTCG-CGCTGTGGAGGGTGTC  6598

Query  4983  TGCTGAGGAGTACGTGGAGGTTACGCGGGTGGGGGATTTCCACTACGTGA-CGGGCATGA  5041
             ||| ||||| ||||||||| | | || ||||||||| ||||||||||| | | ||| |||
Sbjct  6599  TGCAGAGGAATACGTGGAGATAAGGCGGGTGGGGGACTTCCACTACGT-ATCGGGTATGA  6657
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Query  5042  CCACTGACAA-CGTAAAGTGCCCGTGTCAGGTTCCGGCCCCCGAATTCTTCACAGAAGTG  5100
             | |||||||| |  ||||||| ||||||  |||| ||  ||||||||| |||||||| ||
Sbjct  6658  CTACTGACAATCTTAAA-TGCCCGTGCCAGATCCCATCGCCCGAATTTTTCACAGAATTG  6716

Query  5101  GATGGGGTGCGGTTGCACAGGTACGCTCCAGCGTGCAAACCCCTCCTACGGGAGGAGGTC  5160
             || |||||||||  | ||||| ||| ||||||  ||| ||||| ||||| || ||||||
Sbjct  6717  GACGGGGTGCGCCTACACAGGTTTGCGCCCCCTTGCAAGCCCTTGCTGCGGGAGGAGGT-  6775

Query  5161  A-CATTCCTG-TCGGGCTCAATCAA-TACCTGGTTGGGTCACAGCTCCCATGCGAGCCC  5217
             | |||||  | ||  | | |||||| | ||| || |||  || | ||| |||||||||||
Sbjct  6776  ATCATTCA-GAGTAGGACTCCA-CGAGTACCCGGTGGGGTCGCAATTACCTTGCGAGCCC  6833

Query  5218  GAACCGGACGTAGCAGTGCTCACTTCCATGCTCACCGACCCCTCCCACATTACGGCGGAG  5277
             |||||||||||||| ||| | |||||||||||||| ||  |||||||  |  | ||  ||
Sbjct  6834  GAACCGGACGTAGCCGTGTTGACGTCCATGCTCACTGATCCCTCCCATATAACAGCAGAG  6893

Query  5278  ACGGCTAAGCGTAGGCTGGCCAG-GGGATCTCCCCCCTCCT-TGGCCAGCTCATCAGCTA  5335
              | || | | | |||   || || | || | |||   | | | ||||||||| || |||||
Sbjct  6894  GCGGCCGGGAGAAGGTTGGCGAGAGGG-TCACCCCCTTC-TATGGCCAGCTCCTCGGCTA  6951

Query  5336  GCCAGCTGTCTGCGCCTTC-CTTGAAGGCAACATGCACTACCCGTCATGACTCCCCGGAC  5394
             |||||||||| ||| | |  ||| |||||||| |||| ||||| | ||||||||||| ||
Sbjct  6952  GCCAGCTGTCCGCTCCATCTCTC-AAGGCAACTTGCACCGCCAACCATGACTCCCCTGAC  7010

Query  5395  GCTGACCTCATCGAGGCCAACCTCCTGTGGCGGCAGGAGATGGGCGGGAACATCACCCGC  5454
             ||||||||||| || || | |||||||||| |||||||||||||||| |||||||||| |
Sbjct  7011  GCCGAGCTCATAGAGGCTAACCTCCTGTGGAGGCAGGAGATGGGCGGCAACATCACCAGG  7070

Query  5455  GTGGAGTCAGAAAATAAGGTAGTAATTTTGGACTCTTTCGAGCCGCTCCAAGCGGAGGAG  5514
             || ||||||||  | ||| | ||| ||| |||||| || |||||| | |  || ||||||
Sbjct  7071  GTTGAGTCAGAGAACAAAGTGGTGATTCTGGACTCCTTCGATCCGCTTGTGGCAGAGGAG  7130

Query  5515  GATGAGAGGGAAGTATCCGTTCCGGCGGAGATCCTGCGGAGGTC-CAGGAAATTC-CCTC  5572
             ||||| | || ||| | ||| | |||| |||| || ||||| || | |||| || | || |
Sbjct  7131  GATGAGCGGGAGGTCTCCGTACCTGCAGAAATTCTGCGGAAGTCTC-GGAGATTCGCC-C  7188

Query  5573  GAGCGATGCCCATATGGGCACGCCCGGATTACAACCCTCCACT-GTTAGAGTCCTGGAAG  5631
             | || |||| | ||  || ||| | || ||||||||    || | || | || |||||
Sbjct  7189  GGGCCCTGCCCGTCTGGGCGCGGCCGGACTACAACCCCCCGCTAGT-AGAGACGTGGAAA  7247

Query  5632  GACCCGGACTACGTCCCTCCAGTGGTACACGGGTGTCCATTGCCGCCTGCCAAGG-CCCC  5690
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Sbjct  7248  AAGCCTGACTACGAACCACCTGTGGTCCATGGCTGCCCGCTACCACCT-CCACGGTCCCC  7306

Query  5691  TCC-GATACCACCTCCACGGAGGAAGAGGACGGTTGTCCTGTCAGAATCTACCGTGTCTT  5749
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Sbjct  7307  TCCTG-TGCCTCCGCCTCGGAAAAAGCGTACGGTGGTCCTCACCGAATCAACCCTATCTA  7365

Query  5750  CTGCCTTGGCGGAGCTCGCCAC-AAAGACCTTCGGCAGCTCCG-AATCGTC-GGCCGTCG  5806
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Sbjct  7366  CTGCCTTGGCCGAGCTTGCCACCAAA-AGTTTTGGCAGCTCCTCAA-CTTCCGGCATT--  7421

Query  5807  ACAG-CGGCA---CGGCAACGGCCTCTCCTGACCAGCCC-TCC-GACGACGGCGACGCGG  5860
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Sbjct  7422  ACGGGCGACAATACGACAACATCCTCTGA-GCCC-GCCCCTTCTG--G-CTGCCCCCCCG  7476

Query  5861  GA-TCCGACGTTGAGTCGTACTCCTCCATGᴄᴏᴏᴄᴏᴄᴏᴄTTGAGGGGGAGCCGGGGGATCCC  5919
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Sbjct  7477  -ACTCCGACGTTGAGTCCTATTCTTCCATGCCCCCCCTGGAGGGGGAGCCTGGGGATCCG  7535

Query  5920  GATCTCAGCGACGGGTCTTGGTCTACCGTAAGC-GAGGAGGCT-AGT-G-AGGACGTCGT  5975
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Query  6035  AA-ACCAAGCTGCCCATCAATGCACTGAGCAACTCTTTGCTCCGTCACCACAA-CTTGGT  6092
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Query  6093  CTATGCTACAACATCTCGCAGCGCAAGCCTGCGGCAGAAGAAGGTCACCTTTGACAGACT  6152
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Sbjct  7888  CAGCCAAATCCAAGTTTGGCTATGGGGCAAAGACGTCCGTTGCC-ATGCCAGAAAGGCC  7946

Query  6328  GTTAACC-ACATCCGCTCCGTGTGGAAGGAC-TTGCTGGAAGACACTG-AGACACCAATT  6384
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Query  6445  AAGCCAGCTCGCCTTATCGTATTCCCAGATTTGGGGGTTCGTGTGTGCGAGAAAATGGCC  6504
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Query  6620  GCCCTATGGGCTTCGCATATGACACCCGCTGTTTTGACTCAACGGTCACTGAGAATGACA  6679
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Query  6738  CAT-AAGGTCGCTCACAGAGCGGCTTTACATCGGGGGCCCCCTGACTAATTCTAAAGGGC  6796
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Sbjct  8827  TAGGCAACATAATCATGTTTGCCCCCACACT-GTGGGCGAGGATGATACTGATGACCCAT  8885

Query  7267  TTCTTCTC-CATCCTTC-TAGCTCAGGAA-CAACTTGAAAAAGCCCT-AGATTGTCAGAT  7322
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Sbjct  8886  TTCTT-TAGCGTCCT-CATAGC-CAGGGATCAGCTTGAACAGGCTCTTA-ACTGTGAGAT  8941

Query  7323  CTACGGGGCCTGTTACTCCATTGAGCCACTTGACCTACCTC-AGATCATTCAACGACTCC  7381
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Sbjct  9061  CATGCCTCAGAAAACTTGGGGTCCCGCCCTTGCGAG-CTTGGAGACACCGGGCCCGGAGC  9119
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Query  7559  TCAACTGGGCAGTAAGGACCAAGCTCAAACTCACTCCAATCCCGGCTGC-GTCCCAGTTG  7617
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Query  7793  -CCTGttttttccttttttttttttctttttttttttttttttttttttttttttttttt  7851
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Query  7911  TAGTCACGGCTAGCTGTGAAAGGTCCGTGAGCCGCTTGACTGCAGAGAGTGCTGATACTG  7970
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Query  7971  GCCTCTCTGCAGATCA  7986
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Sbjct  9581  GCCTCTCTGCAGATCA  9596


   Score =  664 bits (359),  Expect = 0.0
   Identities = 373/379 (98%),  Gaps = 4/379 (1%)
   Strand=Plus/Plus

Query  1    GCCAGCCCCC-GATTGGGGGCGACACTCCACCATAG-ATCACTCCCCTGTGAGGAACTAC  58
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Sbjct  1    GCCAGCCCCCTGA-TGGGGGCGACACTCCACCAT-GAATCACTCCCCTGTGAGGAACTAC  58

Query  59   TGTCTTCACGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGG  118
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Query  119  AccccccccTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCC  178
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Query  359  ACCTCAAAGAAAAACCAAA  377
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Sbjct  359  ACCTCAAAGAAAAACCAAA  377
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